Connecting via Winsock to STN at pto-stn on port 23

Welcome to STN International! Enter x:X

LOGINID:ssspta1632ras

PASSWORD:
TERMINAL (ENTER 1, 2, 3, OR ?):2

* * * * * * * * * * Welcome to STN International * * * * * * * * * *

NEWS 1		Web Page for STN Seminar Schedule - N. America
NEWS 2	OCT 04	Precision of EMBASE searching enhanced with new chemical name field
NEWS 3	OCT 06	Increase your retrieval consistency with new formats or for Taiwanese application numbers in CA/CAplus.
NEWS 4	OCT 21	CA/CAplus kind code changes for Chinese patents increase consistency, save time
NEWS 5	OCT 22	New version of STN Viewer preserves custom highlighting of terms when patent documents are saved in .rtf format
NEWS 6	OCT 28	INPADOCDB/INPAFAMDB: Enhancements to the US national patent classification.
NEWS 7	NOV 03	New format for Korean patent application numbers in CA/CAplus increases consistency, saves time.
NEWS 8	NOV 04	Selected STN databases scheduled for removal on December 31, 2010
NEWS 9	NOV 18	PROUSDDR and SYNTHLINE Scheduled for Removal December 31, 2010 by Request of Prous Science
NEWS 10	NOV 22	Higher System Limits Increase the Power of STN Substance-Based Searching
NEWS 11	NOV 24	Search an additional 46,850 records with MEDLINE backfile extension to 1946
NEWS 12	DEC 14	New PNK Field Allows More Precise Crossover among STN Patent Databases
NEWS 13	DEC 18	ReaxysFile available on STN
NEWS 14	DEC 21	CAS Learning Solutions -- a new online training experience
NEWS 15	DEC 22	Value-Added Indexing Improves Access to World Traditional Medicine Patents in CAplus
NEWS 16	JAN 24	The new and enhanced DPCI file on STN has been released
NEWS 17	JAN 26	Improved Timeliness of CAS Indexing Adds Value to USPATFULL and USPAT2 Chemistry Patents
NEWS 18	JAN 26	Updated MeSH vocabulary, new structured abstracts, and other enhancements improve searching in STN reload of MEDLINE
NEWS 19	JAN 28	CABA will be updated weekly
NEWS 20	FEB 23	PCTFULL file on STN completely reloaded
NEWS 21	FEB 23	STN AnaVist Test Projects Now Available for Qualified Customers
NEWS 22	FEB 25	LPCI will be replaced by LDPCI
NEWS 23	MAR 07	Pricing for SELECTing Patent, Application, and Priority Numbers in the USPAT and IFI Database Families is Now Consistent with Similar Patent Databases on STN
NEWS 24	APR 26	Expanded Swedish Patent Application Coverage in CA/CAplus Provides More Current and Complete Information
NEWS 25	APR 28	The DWPI (files WPINDEX, WPIDS and WPIX) on STN have been

```
                  enhanced with thesauri for the European Patent Classifications
 NEWS 26  MAY 02  MEDLINE Improvements Provide Fast and Simple Access to DOI and
                  Chemical Name Information
 NEWS 27  MAY 12  European Patent Classification thesauri added to the INPADOC
                  files, PCTFULL, GBFULL and FRFULL
 NEWS 28  MAY 20  PATDPA database updates to end in June 2011
 NEWS 29  MAY 23  STN biosequence searches with enhanced performance
 NEWS 30  MAY 23  Free Trial of the Numeric Property Search Feature
                  in PCTFULL on STN

 NEWS EXPRESS 17 DECEMBER 2010 CURRENT WINDOWS VERSION IS V8.4.2 .1,
          AND CURRENT DISCOVER FILE IS DATED 24 JANUARY 2011.

 NEWS HOURS    STN Operating Hours Plus Help Desk Availability
 NEWS LOGIN    Welcome Banner and News Items

Enter NEWS followed by the item number or name to see news on that
specific topic.

  All use of STN is subject to the provisions of the STN customer
  agreement.  This agreement limits use to scientific research.  Use
  for software development or design, implementation of commercial
  gateways, or use of CAS and STN data in the building of commercial
  products is prohibited and may result in loss of user privileges
  and other penalties.

* * * * * * * * * * * * * * * * STN  Columbus  * * * * * * * * * * * * * * * *

FILE 'HOME' ENTERED AT 10:06:00 ON 25 MAY 2011

=> file medline
COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
                                                         ENTRY    SESSION
FULL ESTIMATED COST                                       0.23       0.23

FILE 'MEDLINE' ENTERED AT 10:06:07 ON 25 MAY 2011

 FILE LAST UPDATED: 24 May 2011 (20110524/UP).  FILE COVERS 1946 TO DATE.

 MEDLINE and LMEDLINE have been updated with the 2011 Medical Subject
 Headings (MeSH) vocabulary and tree numbers from the U.S.  National Library
 of Medicine (NLM).  Additional information is available at:

 http://www.nlm.nih.gov/pubs/techbull/nd10/nd10_medline_data_changes_2011.html.

 The 2011 Medline reload was completed on January 22, 2011.
 See HELP RLOAD for details.

 This file contains CAS Registry Numbers for easy and accurate
 substance identification.

 See HELP RANGE before carrying out any RANGE search.

=> s sequence requirements for micrna processing
        980083 SEQUENCE
        289417 SEQUENCES
       1065959 SEQUENCE
                 (SEQUENCE OR SEQUENCES)
        113931 REQUIREMENTS
       8853374 FOR
            71 FORS
```

```
       8853397 FOR
                 (FOR OR FORS)
             8 MICRNA
             4 MICRNAS
             9 MICRNA
                 (MICRNA OR MICRNAS)
        306533 PROCESSING
            99 PROCESSINGS
        306583 PROCESSING
                 (PROCESSING OR PROCESSINGS)
L1           0 SEQUENCE REQUIREMENTS FOR MICRNA PROCESSING
                 (SEQUENCE(W)REQUIREMENTS(W)FOR(W)MICRNA(W)PROCESSING)

=>  s sequence requirements for microna processing
        980083 SEQUENCE
        289417 SEQUENCES
       1065959 SEQUENCE
                 (SEQUENCE OR SEQUENCES)
        113931 REQUIREMENTS
       8853374 FOR
            71 FORS
       8853397 FOR
                 (FOR OR FORS)
            17 MICRONA
        306533 PROCESSING
            99 PROCESSINGS
        306583 PROCESSING
                 (PROCESSING OR PROCESSINGS)
L2           0 SEQUENCE REQUIREMENTS FOR MICRONA PROCESSING
                 (SEQUENCE(W)REQUIREMENTS(W)FOR(W)MICRONA(W)PROCESSING)

=>  s sequence requirements for micro na processing
        980083 SEQUENCE
        289417 SEQUENCES
       1065959 SEQUENCE
                 (SEQUENCE OR SEQUENCES)
        113931 REQUIREMENTS
       8853374 FOR
            71 FORS
       8853397 FOR
                 (FOR OR FORS)
         62353 MICRO
          3518 MICROS
         65798 MICRO
                 (MICRO OR MICROS)
        252867 NA
          3532 NAS
        255903 NA
                 (NA OR NAS)
        306533 PROCESSING
            99 PROCESSINGS
        306583 PROCESSING
                 (PROCESSING OR PROCESSINGS)
L3           0 SEQUENCE REQUIREMENTS FOR MICRO NA PROCESSING
                 (SEQUENCE(W)REQUIREMENTS(W)FOR(W)MICRO(W)NA(W)PROCESSING)

=>  s sequence requirements for micro rna processing
        980083 SEQUENCE
        289417 SEQUENCES
       1065959 SEQUENCE
                 (SEQUENCE OR SEQUENCES)
```

```
        113931 REQUIREMENTS
       8853374 FOR
            71 FORS
       8853397 FOR
                  (FOR OR FORS)
         62353 MICRO
          3518 MICROS
         65798 MICRO
                  (MICRO OR MICROS)
        628278 RNA
         31663 RNAS
        632468 RNA
                  (RNA OR RNAS)
        306533 PROCESSING
            99 PROCESSINGS
        306583 PROCESSING
                  (PROCESSING OR PROCESSINGS)
L4           1 SEQUENCE REQUIREMENTS FOR MICRO RNA PROCESSING
                  (SEQUENCE(W)REQUIREMENTS(W)FOR(W)MICRO(W)RNA(W)PROCESSING)

=> d bib

L4   ANSWER 1 OF 1     MEDLINE on STN
AN   2003140447     MEDLINE <<LOGINID::20110525>>
DN   PubMed ID: 12554881
TI   Sequence requirements for micro RNA processing and function in
     human cells.
AU   Zeng Yan; Cullen Bryan R
CS   Howard Hughes Medical Institute, Department of Molecular Genetics and
     Microbiology, Duke University Medical Center, Durham, North Carolina
     27710, USA.
SO   RNA (New York, N.Y.), (2003 Jan) Vol. 9, No. 1, pp. 112-23.
     Journal code: 9509184. ISSN: 1355-8382. L-ISSN: 1355-8382.
     Report No.: NLM-PMC1370375.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   200304
ED   Entered STN: 27 Mar 2003
     Last Updated on STN: 17 Apr 2003
     Entered Medline: 16 Apr 2003
OSC.G 63      There are 63 MEDLINE records that cite this record
REM.CNT 29    There are 29 cited references available in MEDLINE for this
              document.


=> d his full

     (FILE 'HOME' ENTERED AT 10:06:00 ON 25 MAY 2011)

     FILE 'MEDLINE' ENTERED AT 10:06:07 ON 25 MAY 2011
L1             0 SEA PLU=ON  SEQUENCE REQUIREMENTS FOR MICRNA PROCESSING
L2             0 SEA PLU=ON  SEQUENCE REQUIREMENTS FOR MICRONA PROCESSING
L3             0 SEA PLU=ON  SEQUENCE REQUIREMENTS FOR MICRO NA PROCESSING
L4             1 SEA PLU=ON  SEQUENCE REQUIREMENTS FOR MICRO RNA PROCESSING
                 D BIB


     FILE HOME
```

FILE MEDLINE
FILE LAST UPDATED: 24 May 2011 (20110524/UP). FILE COVERS 1946 TO DATE.

MEDLINE and LMEDLINE have been updated with the 2011 Medical Subject Headings (MeSH) vocabulary and tree numbers from the U.S. National Libra of Medicine (NLM). Additional information is available at:

http://www.nlm.nih.gov/pubs/techbull/nd10/nd10_medline_data_changes_2011.

The 2011 Medline reload was completed on January 22, 2011.
See HELP RLOAD for details.

This file contains CAS Registry Numbers for easy and accurate substance identification.

See HELP RANGE before carrying out any RANGE search.

=> log y

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	1.04	1.27

STN INTERNATIONAL LOGOFF AT 10:07:26 ON 25 MAY 2011

Connecting via Winsock to STN at pto-stn on port 23

Welcome to STN International! Enter x:X

LOGINID:ssspta1632ras

PASSWORD:
TERMINAL (ENTER 1, 2, 3, OR ?):2

* * * * * * * * * * Welcome to STN International * * * * * * * * * *

NEWS	1		Web Page for STN Seminar Schedule - N. America
NEWS	2	OCT 04	Precision of EMBASE searching enhanced with new chemical name field
NEWS	3	OCT 06	Increase your retrieval consistency with new formats or for Taiwanese application numbers in CA/CAplus.
NEWS	4	OCT 21	CA/CAplus kind code changes for Chinese patents increase consistency, save time
NEWS	5	OCT 22	New version of STN Viewer preserves custom highlighting of terms when patent documents are saved in .rtf format
NEWS	6	OCT 28	INPADOCDB/INPAFAMDB: Enhancements to the US national patent classification.
NEWS	7	NOV 03	New format for Korean patent application numbers in CA/CAplus increases consistency, saves time.
NEWS	8	NOV 04	Selected STN databases scheduled for removal on December 31, 2010
NEWS	9	NOV 18	PROUSDDR and SYNTHLINE Scheduled for Removal December 31, 2010 by Request of Prous Science
NEWS	10	NOV 22	Higher System Limits Increase the Power of STN Substance-Based Searching

```
 NEWS 11  NOV 24  Search an additional 46,850 records with MEDLINE
                  backfile extension to 1946
 NEWS 12  DEC 14  New PNK Field Allows More Precise Crossover among STN
                  Patent Databases
 NEWS 13  DEC 18  ReaxysFile available on STN
 NEWS 14  DEC 21  CAS Learning Solutions -- a new online training experience
 NEWS 15  DEC 22  Value-Added Indexing Improves Access to World Traditional
                  Medicine Patents in CAplus
 NEWS 16  JAN 24  The new and enhanced DPCI file on STN has been released
 NEWS 17  JAN 26  Improved Timeliness of CAS Indexing Adds Value to
                  USPATFULL and USPAT2 Chemistry Patents
 NEWS 18  JAN 26  Updated MeSH vocabulary, new structured abstracts, and
                  other enhancements improve searching in STN reload of
                  MEDLINE
 NEWS 19  JAN 28  CABA will be updated weekly
 NEWS 20  FEB 23  PCTFULL file on STN completely reloaded
 NEWS 21  FEB 23  STN AnaVist Test Projects Now Available for
                  Qualified Customers
 NEWS 22  FEB 25  LPCI will be replaced by LDPCI
 NEWS 23  MAR 07  Pricing for SELECTing Patent, Application, and Priority
                  Numbers in the USPAT and IFI Database Families is Now
                  Consistent with Similar Patent Databases on STN
 NEWS 24  APR 26  Expanded Swedish Patent Application Coverage in CA/CAplus
                  Provides More Current and Complete Information
 NEWS 25  APR 28  The DWPI (files WPINDEX, WPIDS and WPIX) on STN have been
                  enhanced with thesauri for the European Patent Classifications
 NEWS 26  MAY 02  MEDLINE Improvements Provide Fast and Simple Access to DOI and
                  Chemical Name Information
 NEWS 27  MAY 12  European Patent Classification thesauri added to the INPADOC
                  files, PCTFULL, GBFULL and FRFULL
 NEWS 28  MAY 20  PATDPA database updates to end in June 2011
 NEWS 29  MAY 23  STN biosequence searches with enhanced performance
 NEWS 30  MAY 23  Free Trial of the Numeric Property Search Feature
                  in PCTFULL on STN

 NEWS EXPRESS 17 DECEMBER 2010 CURRENT WINDOWS VERSION IS V8.4.2 .1,
          AND CURRENT DISCOVER FILE IS DATED 24 JANUARY 2011.

 NEWS HOURS    STN Operating Hours Plus Help Desk Availability
 NEWS LOGIN    Welcome Banner and News Items

Enter NEWS followed by the item number or name to see news on that
specific topic.

  All use of STN is subject to the provisions of the STN customer
  agreement.  This agreement limits use to scientific research.  Use
  for software development or design, implementation of commercial
  gateways, or use of CAS and STN data in the building of commercial
  products is prohibited and may result in loss of user privileges
  and other penalties.

* * * * * * * * * * * * * * * * STN  Columbus  * * * * * * * * * * * * * * * *

FILE 'HOME' ENTERED AT 06:28:39 ON 26 MAY 2011

=> file medline
COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
                                                       ENTRY    SESSION
FULL ESTIMATED COST                                     0.23       0.23

FILE 'MEDLINE' ENTERED AT 06:28:50 ON 26 MAY 2011
```

FILE LAST UPDATED: 25 May 2011 (20110525/UP). FILE COVERS 1946 TO DATE.

MEDLINE and LMEDLINE have been updated with the 2011 Medical Subject Headings (MeSH) vocabulary and tree numbers from the U.S. National Library of Medicine (NLM). Additional information is available at:

http://www.nlm.nih.gov/pubs/techbull/nd10/nd10_medline_data_changes_2011.html.

The 2011 Medline reload was completed on January 22, 2011.
See HELP RLOAD for details.

This file contains CAS Registry Numbers for easy and accurate substance identification.

See HELP RANGE before carrying out any RANGE search.

```
=> s (mirna or microrna or micro rna) response element
MISSING OPERATOR RNA) RESPONSE
The search profile that was entered contains terms or
nested terms that are not separated by a logical operator.

=> s (mirna or microrna or micro rna) (1a) response element
          5493 MIRNA
          5426 MIRNAS
          6704 MIRNA
                 (MIRNA OR MIRNAS)
          6307 MICRORNA
         10014 MICRORNAS
         10846 MICRORNA
                 (MICRORNA OR MICRORNAS)
         62372 MICRO
          3518 MICROS
         65817 MICRO
                 (MICRO OR MICROS)
        628399 RNA
         31668 RNAS
        632588 RNA
                 (RNA OR RNAS)
           505 MICRO RNA
                 (MICRO(W)RNA)
       1469438 RESPONSE
        531522 RESPONSES
       1763118 RESPONSE
                 (RESPONSE OR RESPONSES)
        114998 ELEMENT
        204235 ELEMENTS
        284466 ELEMENT
                 (ELEMENT OR ELEMENTS)
         24035 RESPONSE ELEMENT
                 (RESPONSE(W)ELEMENT)
L1           8 (MIRNA OR MICRORNA OR MICRO RNA) (1A) RESPONSE ELEMENT

=> d bib ab 1-8

L1   ANSWER 1 OF 8     MEDLINE on STN
AN   2011350953     IN-PROCESS <<LOGINID::20110526>>
DN   PubMed ID: 21310851
TI   MicroRNA hsa-miR-613 targets the human LXRα gene and mediates a
     feedback loop of LXRα autoregulation.
AU   Ou Zhimin; Wada Taira; Gramignoli Roberto; Li Song; Strom Stephen C; Huang
```

Min; Xie Wen
CS Center for Pharmacogenetics, Department of Pharmaceutical Sciences, University of Pittsburgh, Pittsburgh, Pennsylvania 15261, USA.
NC DK076962 (United States NIDDK NIH HHS)
ES014626 (United States NIEHS NIH HHS)
SO Molecular endocrinology (Baltimore, Md.), (2011 Apr) Vol. 25, No. 4, pp. 584-96. Electronic Publication: 2011-02-10.
Journal code: 8801431. E-ISSN: 1944-9917. L-ISSN: 0888-8809.
Report No.: NLM-PMC3063084 [Available on 04/01/12].
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, N.I.H., EXTRAMURAL)
(RESEARCH SUPPORT, NON-U.S. GOV'T)
LA English
FS NONMEDLINE; IN-PROCESS; NONINDEXED; Priority Journals
ED Entered STN: 31 Mar 2011
Last Updated on STN: 13 May 2011
AB The nuclear receptor liver X receptor (LXR) is a ligand-dependent transcription factor that plays an important role in the metabolism and homeostasis of cholesterol, lipids, bile acids, and steroid hormones. MicroRNAs (miRNAs) are recently recognized important negative regulators of gene expression. In this report, we showed that miRNA hsa-miR-613 played an important role in the autoregulation of the human LXRα gene. hsa-miR-613 targeted the endogenous LXRα through its specific miRNA response element (613MRE) within the LXRα 3'-untranslated region. Interestingly and paradoxically, the expression of hsa-miR-613 itself was induced upon the activation of LXR. However, hsa-miR-613 did not appear to be a direct LXR target gene. Instead, the positive regulation of hsa-miR-613 by LXR was mediated by the sterol regulatory element binding protein (SREBP)-1c, a known LXR target gene. Promoter analysis revealed an SREBP response element in the hsa-miR-613 gene promoter. Treatment with insulin also induced the expression of hsa-miR-613 in an SREBP-1c-dependent manner, further supporting the role of SREBP-1c in the positive regulation of this miRNA species. Finally, the autoinduction of LXRα by a LXR agonist was enhanced when hsa-miR-613 was inhibited or SREBP-1c was down-regulated. hsa-miR-613 appeared to specifically target the human LXRα. We propose that the negative regulation mediated by hsa-miR-613 and SREBP-1c and the previously reported positive regulation mediated by an LXR response element in the LXRα gene promoter constitute a ying-yang mechanism to ensure a tight regulation of this nuclear receptor of many metabolic functions.

L1 ANSWER 2 OF 8 MEDLINE on STN
AN 2011201873 MEDLINE <<LOGINID::20110526>>
DN PubMed ID: 21219875
TI Breast cancer resistance protein BCRP/ABCG2 regulatory microRNAs (hsa-miR-328, -519c and -520h) and their differential expression in stem-like ABCG2+ cancer cells.
AU Li Xin; Pan Yu-Zhuo; Seigel Gail M; Hu Zi-Hua; Huang Min; Yu Ai-Ming
CS Department of Pharmaceutical Sciences, University at Buffalo, The State University of New York, Buffalo, NY 14260-1200, USA.
NC R01 DA021172-04 (United States NIDA NIH HHS)
R01DA021172 (United States NIDA NIH HHS)
R21CA127061 (United States NCI NIH HHS)
U54CA143876 (United States NCI NIH HHS)
SO Biochemical pharmacology, (2011 Mar 15) Vol. 81, No. 6, pp. 783-92. Electronic Publication: 2011-01-08.
Journal code: 0101032. E-ISSN: 1873-2968. L-ISSN: 0006-2952.
Report No.: NLM-NIHMS264683 [Available on 03/15/12]; NLM-PMC3042498 [Available on 03/15/12].

CY England: United Kingdom
DT (COMPARATIVE STUDY)
Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, N.I.H., EXTRAMURAL)
(RESEARCH SUPPORT, NON-U.S. GOV'T)
LA English
FS Priority Journals
EM 201104
ED Entered STN: 22 Feb 2011
Last Updated on STN: 19 Apr 2011
Entered Medline: 18 Apr 2011
AB Recent studies have shown that a number of microRNAs (miRNA or miR) may regulate human breast cancer resistance protein (BCRP/ABCG2), an important efflux transporter responsible for cellular drug disposition, whereas their effects on ABCG2 protein expression are not compared. In this study, we first identified a new proximal miRNA response element (MRE) for hsa-miR-519c within ABCG2 3'-untranslated region (3'UTR) through computational analyses. This miR-519c MRE site was confirmed using dual luciferase reporter assay and site-directed mutagenesis. Immunoblot analyses indicated that ABCG2 protein expression was significantly down-regulated in MCF-7/MX100 cells after transfection with hsa-miR-328- or -519c expression plasmids, and was markedly up-regulated in MCF-7 cells after transfection with miR-328 or -519c antagomir. However, ABCG2 protein expression was unchanged in MCF-7/MX100 cells after transfection with hsa-miR-520h expression plasmids, which was associated with undetectable miR-520h expression. Furthermore, ABCG2 mRNA degradation was accelerated dramatically in cells transfected with miR-519c expression plasmid, suggesting the involvement of mRNA degradation mechanism. Intervention of miR-328 or -519c signaling led to significant change in intracellular mitoxantrone accumulation, as determined by flow cytometry analyses. In addition, we separated RB143 human retinoblastoma cells into stem-like (ABCG2+) and non-stem-like (ABCG2-) populations through immunomagnetic selection, and found that miR-328, -519c and -520h levels were 9-, 15- and 3-fold lower in the ABCG2+ cells, respectively. Our data suggest that miR-519c and -328 have greater impact on ABCG2 expression than miR-520h in MCF-7 human breast cancer cells, and the presence of proximal miR-519c MRE explains the action of miR-519c on shortened ABCG2 3'UTR.

L1 ANSWER 3 OF 8 MEDLINE on STN
AN 2011141520 IN-PROCESS <<LOGINID::20110526>>
DN PubMed ID: 21264258
TI Role of microRNA-26b in glioma development and its mediated regulation on EphA2.
AU Wu Ning; Zhao Xiangzhong; Liu Ming; Liu Haizhou; Yao Weicheng; Zhang Yuyan; Cao Shousong; Lin Xiukun
CS Institute of Oceanology, Chinese Academy of Sciences, Qingdao, China.
SO PloS one, (2011) Vol. 6, No. 1, pp. e16264. Electronic Publication: 2011-01-14.
Journal code: 101285081. E-ISSN: 1932-6203. L-ISSN: 1932-6203.
Report No.: NLM-PMC3021542.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, NON-U.S. GOV'T)
LA English
FS NONMEDLINE; IN-PROCESS; NONINDEXED; Priority Journals
ED Entered STN: 26 Jan 2011
Last Updated on STN: 17 Feb 2011
AB BACKGROUND: MicroRNAs (miRNAs) are short, non-coding RNAs that regulate the expression of multiple target genes. Deregulation of miRNAs is common

in human tumorigenesis. Low level expression of miR-26b has been found in glioma cells. However, its underlying mechanism of action has not been determined.

METHODOLOGY/PRINCIPAL FINDINGS: Real-time PCR was employed to measure the expression level of miR-26b in glioma patients and cells. The level of miR-26b was inversely correlated with the grade of glioma. Ectopic expression of miR-26b inhibited the proliferation, migration and invasion of human glioma cells. A binding site for miR-26b was identified in the 3'UTR of EphA2. Over-expression of miR-26b in glioma cells repressed the endogenous level of EphA2 protein. Vasculogenic mimicry (VM) experiments were performed to further confirm the effects of miR-26b on the regulation of EphA2, and the results showed that miR-26b inhibited the VM processes which regulated by EphA2.

SIGNIFICANCE: This study demonstrated that miR-26b may act as a tumor suppressor in glioma and it directly regulates EphA2 expression. EphA2 is a direct target of miR-26b, and the down-regulation of EphA2 mediated by miR-26b is dependent on the binding of miR-26b to a specific response element of microRNA in the 3'UTR region of EphA2 mRNA.

L1 ANSWER 4 OF 8 MEDLINE on STN
AN 2009633266 MEDLINE <<LOGINID::20110526>>
DN PubMed ID: 19581388
TI MicroRNAs regulate CYP3A4 expression via direct and indirect targeting.
AU Pan Yu-Zhuo; Gao Wenqing; Yu Ai-Ming
CS Department of Pharmaceutical Sciences, School of Pharmacy and Pharmaceutical Sciences, University at Buffalo, The State University of New York, Buffalo, NY 14260-1200, USA.
NC R01-DA021172 (United States NIDA NIH HHS)
SO Drug metabolism and disposition: the biological fate of chemicals, (2009 Oct) Vol. 37, No. 10, pp. 2112-7. Electronic Publication: 2009-07-06. Journal code: 9421550. E-ISSN: 1521-009X. L-ISSN: 0090-9556. Report No.: NLM-PMC2769037.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, N.I.H., EXTRAMURAL)
(RESEARCH SUPPORT, NON-U.S. GOV'T)
LA English
FS Priority Journals
EM 201001
ED Entered STN: 22 Sep 2009
Last Updated on STN: 19 Jan 2010
Entered Medline: 18 Jan 2010
AB CYP3A4 metabolizes many drugs on the market. Although transcriptional regulation of CYP3A4 is known to be tightly controlled by some nuclear receptors (NR) including vitamin D receptor (VDR/NR1I1), posttranscriptional regulation of CYP3A4 remains elusive. In this study, we show that noncoding microRNAs (miRNAs) may control posttranscriptional and transcriptional regulation of CYP3A4 by directly targeting the 3'-untranslated region (3'UTR) of CYP3A4 and indirectly targeting the 3'UTR of VDR, respectively. Luciferase reporter assays showed that CYP3A4 3'UTR-luciferase activity was significantly decreased in human embryonic kidney 293 cells transfected with plasmid that expressed microRNA-27b (miR-27b) or mouse microRNA-298 (mmu-miR-298), whereas the activity was unchanged in cells transfected with plasmid that expressed microRNA-122a or microRNA-328. Disruption of the corresponding miRNA response element (MRE) within CYP3A4 3'UTR led to a 2- to 3-fold increase in luciferase activity. Immunoblot analyses indicated that CYP3A4 protein was down-regulated over 30% by miR-27b and mmu-miR-298 in LS-180 and PANC1 cells. The decrease in CYP3A4 protein expression was associated with

significantly decreased CYP3A4 mRNA levels, as determined by quantitative real-time PCR (qPCR) analyses. Likewise, interactions of miR-27b or mmu-miR-298 with VDR 3'UTR were supported by luciferase reporter assays. The mmu-miR-298 MRE site is well conserved within the 3'UTR of mouse, rat, and human VDR. Down-regulation of VDR by the two miRNAs was supported by immunoblot and qPCR analyses. Furthermore, overexpression of miR-27b or mmu-miR-298 in PANC1 cells led to a lower sensitivity to cyclophosphamide. Together, these findings suggest that CYP3A4 gene expression may be regulated by miRNAs at both the transcriptional and posttranscriptional level.

L1 ANSWER 5 OF 8 MEDLINE on STN
AN 2009614469 MEDLINE <<LOGINID::20110526>>
DN PubMed ID: 19635812
TI MicroRNA-125b promotes neuronal differentiation in human cells by repressing multiple targets.
AU Le Minh T N; Xie Huangming; Zhou Beiyan; Chia Poh Hui; Rizk Pamela; Um Moonkyoung; Udolph Gerald; Yang Henry; Lim Bing; Lodish Harvey F
CS Whitehead Institute for Biomedical Research, 9 Cambridge Center, Suite 601, Cambridge, MA 02142, USA.
NC AI54973 (United States NIAID NIH HHS)
DK047636 (United States NIDDK NIH HHS)
R01 DK068348 (United States NIDDK NIH HHS)
SO Molecular and cellular biology, (2009 Oct) Vol. 29, No. 19, pp. 5290-305.
Electronic Publication: 2009-07-27.
Journal code: 8109087. E-ISSN: 1098-5549. L-ISSN: 0270-7306.
Report No.: NLM-PMC2747988.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, N.I.H., EXTRAMURAL)
(RESEARCH SUPPORT, NON-U.S. GOV'T)
(VALIDATION STUDIES)
LA English
FS Priority Journals
EM 200910
ED Entered STN: 12 Sep 2009
Last Updated on STN: 3 Oct 2009
Entered Medline: 2 Oct 2009
OSC.G 1 There are 1 MEDLINE records that cite this record
REM.CNT 41 There are 41 cited references available in MEDLINE for this document.
AB MicroRNAs (miRNAs) are a class of small noncoding RNAs that regulate gene expression at the posttranscriptional level. Research on miRNAs has highlighted their importance in neural development, but the specific functions of neurally enriched miRNAs remain poorly understood. We report here the expression profile of miRNAs during neuronal differentiation in the human neuroblastoma cell line SH-SY5Y. Six miRNAs were significantly upregulated during differentiation induced by all-trans-retinoic acid and brain-derived neurotrophic factor. We demonstrated that the ectopic expression of either miR-124a or miR-125b increases the percentage of differentiated SH-SY5Y cells with neurite outgrowth. Subsequently, we focused our functional analysis on miR-125b and demonstrated the important role of this miRNA in both the spontaneous and induced differentiations of SH-SH5Y cells. miR-125b is also upregulated during the differentiation of human neural progenitor ReNcell VM cells, and miR-125b ectopic expression significantly promotes the neurite outgrowth of these cells. To identify the targets of miR-125b regulation, we profiled the global changes in gene expression following miR-125b ectopic expression in SH-SY5Y cells. miR-125b represses 164 genes that contain the seed match sequence of the miRNA and/or that are predicted to be direct targets of miR-125b by conventional methods. Pathway analysis suggests that a subset of

miR-125b-repressed targets antagonizes neuronal genes in several neurogenic pathways, thereby mediating the positive effect of miR-125b on neuronal differentiation. We have further validated the binding of miR-125b to the miRNA response elements of 10 selected mRNA targets. Together, we report here for the first time the important role of miR-125b in human neuronal differentiation.

L1 ANSWER 6 OF 8 MEDLINE on STN
AN 2009405411 MEDLINE <<LOGINID::20110526>>
DN PubMed ID: 19483680
TI MicroRNA-mediated species-specific attenuation of influenza A virus.
AU Perez Jasmine T; Pham Alissa M; Lorini Maria H; Chua Mark A; Steel John; tenOever Benjamin R
CS Microbiology Graduate School Training Program, Mount Sinai School of Medicine, New York, New York, USA.
NC T32AI007647-09 (United States NIAID NIH HHS)
SO Nature biotechnology, (2009 Jun) Vol. 27, No. 6, pp. 572-6. Electronic Publication: 2009-05-31.
Journal code: 9604648. E-ISSN: 1546-1696. L-ISSN: 1087-0156.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, N.I.H., EXTRAMURAL)
(RESEARCH SUPPORT, NON-U.S. GOV'T)
(RESEARCH SUPPORT, U.S. GOV'T, NON-P.H.S.)
LA English
FS Priority Journals
EM 200909
ED Entered STN: 11 Jun 2009
Last Updated on STN: 30 Sep 2009
Entered Medline: 29 Sep 2009
OSC.G 1 There are 1 MEDLINE records that cite this record
AB Influenza A virus leads to yearly epidemics and sporadic pandemics. Present prophylactic strategies focus on egg-grown, live, attenuated influenza vaccines (LAIVs), in which attenuation is generated by conferring temperature sensitivity onto the virus. Here we describe an alternative approach to attenuating influenza A virus based on microRNA-mediated gene silencing. By incorporating nonavian microRNA response elements (MREs) into the open-reading frame of the viral nucleoprotein, we generate reassortant LAIVs for H1N1 and H5N1 that are attenuated in mice but not in eggs. MRE-based LAIVs show a greater than two-log reduction in mortality compared with control viruses lacking MREs and elicit a diverse antibody response. This approach might be combined with existing LAIVs to increase attenuation and improve vaccine safety.

L1 ANSWER 7 OF 8 MEDLINE on STN
AN 2009251472 MEDLINE <<LOGINID::20110526>>
DN PubMed ID: 19293287
TI MicroRNA-125b is a novel negative regulator of p53.
AU Le Minh T N; Teh Cathleen; Shyh-Chang Ng; Xie Huangming; Zhou Beiyan; Korzh Vladimir; Lodish Harvey F; Lim Bing
CS Computation and Systems Biology, Singapore-Massachusetts Institute of Technology Alliance, Singapore.
NC AI54973 (United States NIAID NIH HHS)
DK47636 (United States NIDDK NIH HHS)
R01 DK068348 (United States NIDDK NIH HHS)
SO Genes & development, (2009 Apr 1) Vol. 23, No. 7, pp. 862-76. Electronic
Publication: 2009-03-17.
Journal code: 8711660. E-ISSN: 1549-5477. L-ISSN: 0890-9369.
Report No.: NLM-PMC2666337.
CY United States

DT Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, N.I.H., EXTRAMURAL)
(RESEARCH SUPPORT, NON-U.S. GOV'T)
LA English
FS Priority Journals
EM 200904
ED Entered STN: 3 Apr 2009
Last Updated on STN: 16 Apr 2009
Entered Medline: 15 Apr 2009
OSC.G 8 There are 8 MEDLINE records that cite this record
REM.CNT 51 There are 51 cited references available in MEDLINE for this document.
AB The p53 transcription factor is a key tumor suppressor and a central regulator of the stress response. To ensure a robust and precise response to cellular signals, p53 gene expression must be tightly regulated from the transcriptional to the post-translational levels. Computational predictions suggest that several microRNAs are involved in the post-transcriptional regulation of p53. Here we demonstrate that miR-125b, a brain-enriched microRNA, is a bona fide negative regulator of p53 in both zebrafish and humans. miR-125b-mediated down-regulation of p53 is strictly dependent on the binding of miR-125b to a microRNA response element in the 3' untranslated region of p53 mRNA. Overexpression of miR-125b represses the endogenous level of p53 protein and suppresses apoptosis in human neuroblastoma cells and human lung fibroblast cells. In contrast, knockdown of miR-125b elevates the level of p53 protein and induces apoptosis in human lung fibroblasts and in the zebrafish brain. This phenotype can be rescued significantly by either an ablation of endogenous p53 function or ectopic expression of miR-125b in zebrafish. Interestingly, miR-125b is down-regulated when zebrafish embryos are treated with gamma-irradiation or camptothecin, corresponding to the rapid increase in p53 protein in response to DNA damage. Ectopic expression of miR-125b suppresses the increase of p53 and stress-induced apoptosis. Together, our study demonstrates that miR-125b is an important negative regulator of p53 and p53-induced apoptosis during development and during the stress response.

L1 ANSWER 8 OF 8 MEDLINE on STN
AN 2007527050 MEDLINE <<LOGINID::20110526>>
DN PubMed ID: 17689888
TI Comparative analysis of the SBP-box gene families in P. patens and seed plants.
AU Riese Maike; Hohmann Susanne; Saedler Heinz; Munster Thomas; Huijser Peter
CS Max Planck Institute for Plant Breeding Research, Cologne, Germany.
SO Gene, (2007 Oct 15) Vol. 401, No. 1-2, pp. 28-37. Electronic Publication: 2007-07-10.
Journal code: 7706761. ISSN: 0378-1119. L-ISSN: 0378-1119.
CY Netherlands
DT (COMPARATIVE STUDY)
Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200710
ED Entered STN: 11 Sep 2007
Last Updated on STN: 25 Oct 2007
Entered Medline: 24 Oct 2007
OSC.G 6 There are 6 MEDLINE records that cite this record
AB To come to a better understanding of the evolution and function of the SBP-box transcription factor family in plants, we identified, isolated and characterized 13 of its members from the moss Physcomitrella patens. For the majority of the moss SBP-box genes, clear orthologous relationships with family members of flowering plants could be established by

phylogenetic analysis based on the conserved DNA-binding SBP-domain, as well as additional synapomorphic molecular characters. The P. patens SBP-box genes cluster in four separable groups. One of these consists exclusively of moss genes; the three others are shared with family members of Arabidopsis and rice. Besides the family defining DNA-binding SBP-domain, other features can be found conserved between moss and other plant SBP-domain proteins. An AHA-like motif conserved from the unicellular alga Chlamydomonas reinhardtii to flowering plants, was found able to promote transcription in a heterologous yeast system. The conservation of a functional microRNA response element in the mRNA of three of the moss SBP-box genes supports the idea of an ancient origin of microRNA dependent regulation of SBP-box gene family members. As our current knowledge concerning the roles of SBP-box genes in plant development is scarce and the model system P. patens allows targeted mutation, the material we isolated and characterized will be helpful to generate the mutant phenotypes necessary to further elucidate these roles.

=> d his full

(FILE 'HOME' ENTERED AT 06:28:39 ON 26 MAY 2011)

FILE 'MEDLINE' ENTERED AT 06:28:50 ON 26 MAY 2011
L1 8 SEA PLU=ON (MIRNA OR MICRORNA OR MICRO RNA) (1A) RESPONSE ELEMENT
D BIB AB 1-8

FILE HOME

FILE MEDLINE
FILE LAST UPDATED: 25 May 2011 (20110525/UP). FILE COVERS 1946 TO DATE.

MEDLINE and LMEDLINE have been updated with the 2011 Medical Subject Headings (MeSH) vocabulary and tree numbers from the U.S. National Libra of Medicine (NLM). Additional information is available at:

http://www.nlm.nih.gov/pubs/techbull/nd10/nd10_medline_data_changes_2011.

The 2011 Medline reload was completed on January 22, 2011.
See HELP RLOAD for details.

This file contains CAS Registry Numbers for easy and accurate substance identification.

See HELP RANGE before carrying out any RANGE search.

=> log y

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	3.34	3.57

STN INTERNATIONAL LOGOFF AT 06:30:34 ON 26 MAY 2011